```
                    GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:           December 19, 2002, 14:59:02 ; Search time 38 Seconds
                  (without alignments)
                  3074.440 Million cell updates/sec

Title:            US-08-813-323B-1
Perfect score:    2994
Sequence:         1 MESSKKMDAAGTLQPNPPLK..............IKDDTIFIKVIVDTSDLPDP 567

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5
Searched:         671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:    671580

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                 Listing first 45 summaries

Database :        SPTREMBL_21:*
    1: sp_archea:*
    2: sp_bacteria:*
    3: sp_fungi:*
    4: sp_human:*
    5: sp_invertebrate:*
    6: sp_mammal:*
    7: sp_mhc:*
    8: sp_organelle:*
    9: sp_phage:*
   10: sp_plant:*
   11: sp_rodent:*
   12: sp_virus:*
   13: sp_vertebrate:*
   14: sp_unclassified:*
   15: sp_rvirus:*
   16: sp_bacteriap:*
   17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	1243	41.5	558	11	Q61480	Q61480 mus musculu
2	1243	41.5	558	11	P70191	P70191 mus musculu
3	1189.5	39.7	557	4	O00463	O00463 homo sapien
4	832	27.8	508	11	O54896	O54896 mus musculu
5	727.5	24.3	447	4	Q96NT2	Q96nt2 homo sapien
6	708	23.6	501	13	Q90WT6	Q90wt6 carassius a
7	560.5	18.7	470	4	Q9BU24	Q9bu24 homo sapien
8	556.5	18.6	470	4	O14848	O14848 homo sapien
9	548	18.3	522	4	Q9Y4K3	Q9y4k3 homo sapien
10	535	17.9	530	11	P70196	P70196 mus musculu
11	523.5	17.5	462	5	Q9BIW7	Q9biw7 caenorhabdi
12	523.5	17.5	509	5	O62248	O62248 caenorhabdi
13	521.5	17.4	470	11	Q61382	Q61382 mus musculu
14	500	16.7	412	5	Q9UAC5	Q9uac5 drosophila
15	500	16.7	486	5	Q9XYR0	Q9xyr0 drosophila
16	434.5	14.5	352	6	Q95LR1	Q95lr1 macaca fasc

```
17  291    9.7   296   12  Q8QUJ9    Q8quj9 infectious
18  287    9.6   452    5  Q960H6    Q960h6 drosophila
19  274.5  9.2   475    5  Q9UAC4    Q9uac4 drosophila
20  272.5  9.1   463    5  Q9XYQ9    Q9xyq9 drosophila
21  272.5  9.1   475    5  Q9W3I9    Q9w3i9 drosophila
22  263    8.8   395    5  Q9VXG5    Q9vxg5 drosophila
23  206.5  6.9   198    4  O75615    O75615 homo sapien
24  205    6.8   360    4  Q96CC2    Q96cc2 homo sapien
25  204.5  6.8   1063   11  Q9GY55    Q9gy55 mus musculu
26  204    6.8   1098   4   Q90V55    Q90y55 homo sapien
27  203    6.8   239   11  Q9UPQ7    Q9upq7 homo sapien
28  203    6.8   594    4   Q9CQ29    Q9cq29 mus musculu
29  199    6.6   594    4   Q9H073    Q9h073 homo sapien
30  185    6.2   528   13  Q922B6    Q922b6 mus musculu
31  182.5  6.1   335    5  Q91885    Q91885 xenopus lae
32  176    5.9   891    4   Q9N586    Q9n586 caenorhabdi
33  167    5.6   33     4  Q9Y2K3    Q9y2k3 homo sapien
34  165    5.5   626   11  Q9UNL1    Q9unl1 homo sapien
35  157.5  5.3   671   11  Q922N9    Q922n9 mus musculu
36  157    5.3   713   11  Q8R2Q5    Q8r2q5 mus musculu
37  156.5  5.2   1210  11  Q9YHD6    Q9yhd6 rana catesb
38  156.5  5.2   2238  11  Q91VW5    Q91vw5 mus musculu
39  155.5  5.2   609   13  O70365    O70365 xenopus lae
40  155    5.2   390   11  Q92021    Q92021 mus musculu
41  155    5.2   846   10  Q9VSW7    Q9vsw7 drosophila
42  155    5.2   1676  10  O75130    O75130 homo sapien
43  154    5.1   410   16  O23332    O23332 arabidopsis
44  154    5.1   1938  13  O8XL13    O8xl13 clostridium
45  153.5  5.1   1937  13  Q91BD4    Q91bd4 gallus gall
```

RESULT 1
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ID        Q61480
AC        Q61480;
DT        01-NOV-1996 (TrEMBLrel. 01, Created)
DT        01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT        01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE        TRAF5.
GN        TRAF5.
OS        Mus musculus (Mouse).
OC        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX        NCBI_TaxID=10090;
RN        [1]
RP        SEQUENCE FROM N.A.
RC        STRAIN=BALB/c;
RX        MEDLINE=96278943; PubMed=8663299;
RA        Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA        Yagita H., Okumura K.;
RT        "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT        the lymphotoxin-beta receptor";
RL        J. Biol. Chem. 271:14661-14664(1996).
CC        -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR        EMBL; D78141; BAA11218.1; -.
DR        MGD; MGI:107548; Traf5.
DR        InterPro; IPR002083; TRAF.
DR        InterPro; IPR003007; MATH.
DR        InterPro; IPR001841; Znf_ring.
DR        InterPro; IPR001293; Znf_TRAF.
DR        Pfam; PF00917; MATH; 1.
DR        Pfam; PF00917; zf-C3HC4; 1.
DR        Pfam; PF02176; zf-TRAF; 2.
DR        SMART; SM00061; MATH; 1.
DR        SMART; SM00184; RING; 1.
DR        PROSITE; PS00518; ZF_RING_1; 1.
KW        Zinc-finger.
SQ        SEQUENCE  558 AA;  64154 MW;  D85E48674622SD42 CRC64;
```

PRELIMINARY;   PRT;   558 AA.

ALIGNMENTS

Query Match   41.5%;   Score 1243; DB 11; Length 558;

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Best Local Similarity 43.2%;    Pred. No. 8.5e-70;   Mismatches 158;   Indels 48;   Gaps 8;
Conservative 106;
Matches 237;

Qy   41  KFVKTVEDKYKCEKCRLVLCNPKQTECGHRFCESCMAALLS-SSSPKCTACQESIIKDKV   99
             :||  ||  || |||  | || :|  ||| | ||  :|   :|||| |:| || | |
Db   34  QFVEQLEERYKCAFCHSVLHNPHQTGGGHRFCQQCIRSLRELNSVPICPVDKEVIKPQEV   93

Qy  100  FKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRK  159
         |||||||||::| ::||| |  |||  :| | |  :|  | :| |  :|| || || |||
Db   94  FKDNCCKREVLNLHVYCKN-APGCNARIILGRFQDHLQH-CSFQAVPCPNESCREAMLRK  151

Qy  160  DLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVWSCPHKCSVQTLLRSELSA  219
         |::: : |:|: ||| | | || | ::: |::|:|:: || |  | ::| | :|
Db  152  DVKEHLSAYCRFREEKCLYCKRDIVVTNLQDHEENSCPAYPVYSCPNRC-VQTIPRARVNE 210

Qy  220  HLSECVNAPSTCSFKRYGCVFQGTNQOIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNE  279
         || | | | || ||||||  |: ||: |||:|:| |:|| | || ||: :|  ||  :
Db  211  HLTVCPEAEQDCPFKHYGCTVKGKRGNLLEHRAALQDHMLLVLEKNYQLEQRISDLYQS   270

Qy  280  SVEKNKSIQSLHNQICSFEIEIERQKEMLRNN------------------ESKILHLQ   319
         :::|:||| |  |::   |  |:|  |:|                      :|  | ||
Db  271  LEQKESKIQQLAETVKKFEKELKQFTQMFGRNGTFLSNVQALTSHTDKSAWLEAQVRHLL  330

Qy  320  RVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGL  379
            :  |
Db  331  QIVNQQPSRL------------DLRSLVDAVDSVKQRITQLEASD------QRLVL     368

Qy  380  LESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSL  439
         || | | || :  | |  : :|:|| | | | | :|||| :|| ::|:|:||  | | |:
Db  369  LEGETSKHDAHINHKAQLNKNEERFKQLEGACYSGKLIWKVTDYRVKKREAVEGHTVSV   428

Qy  440  YSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMD  499
         :|||||| : |: |||:|||||| |||||||||:||: |||:|:||:|||:|:||||| |
Db  429  FSQPFYTSRCGYRLCARAYLNGDGSGKGTHLSLYFVVWRGEFDSLLQWPFRQRVTLMLLD  488

Qy  500  QGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN---GTYIKDDTIFIKV 557
         | | ::|:  :| ||||||||:| ||||||||||:||:: :||||   :|||||||:|:||
Db  489  QSGKKNHIVETFKADPNSSSFKRPDGEMNIASGCPRFVSHSTLENSKNTYIKDDTLFLKV  548

Qy  558  IVDTSDLPD  566
         :||::|::|
Db  549  AVDLTDLED  557
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RESULT 2
ID   P70191
AC   P70191;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF5 (Similar to TNF receptor-associated factor 5).
GN   TRAF5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9638484; PubMed=8790348;
RA   Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
RA   Yamamoto T., Inoue J.;
RT   "TRAF5, a novel tumor necrosis factor receptor-associated factor
RT   family protein, mediates CD40 signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
DR   EMBL; D83528; BAA11942.1; -.

DR   MGD; MGI:107548; Traf5.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003107; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE 558 AA; 64145 MW; 48F64FB83BD587E5 CRC64;

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Query Match    Best Local Similarity 41.5%;   Pred. No. 8.5e-70;   Mismatches 168;   Indels 20;   Gaps 9;
Conservative 108;
Matches 239;
Score 1243;   DB 11;   Length 558;

Qy   41  KFVKTVEDKYKCEKCRLVLCNPKQTECGHRFCESCMAALLS-SSSPKCTACQESIIKDKV   99
             :||  ||  || |||  | || :|  ||| | ||  :|   :|||| |:| || | |
Db   34  QFVEQLEERYKCAFCHSVLHNPHQTGGGHRFCQQCIRSLRELNSVPICPVDKEVIKPQEV   93

Qy  100  FKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRK  159
         |||||||||::| ::||| |  |||  :| | |  :|  | :| |  :|| || || |||
Db   94  FKDNCCKREVLNLHVYCKN-APGCNARIILGRFQDHLQH-CSFQAVPCPNESCREAMLRK  151

Qy  160  DLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVWSCPHKCSVQTLLRSELSA  219
         |::: : |:|: ||| | | || | ::: |::|:|:: || |  | ::| | :|
Db  152  DVKEHLSAYCRFREEKCLYCKRDIVVTNLQDHEENSCPAYPVYSCPNRC-VQTIPRARVNE 210

Qy  220  HLSECVNAPSTCSFKRYGCVFQGTNQOIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNE  279
         || | | | || ||||||  |: ||: |||:|:| |:|| | || ||: :|  ||  :
Db  211  HLTVCPEAEQDCPFKHYGCTVKGKRGNLLEHRAALQDHMLLVLEKNYQLEQRISDLYQS   270

Qy  280  SVEKNKSIQSLHNQICSFEIEIERQKEMLRNN---GTYIKDDTIFIKV------         329
         :::|:||| |  |::   |  |:|  |:|
Db  271  LEQKESKIQQLAETVKKFEKELKQFTQMFGRNGTFLSNVQ-ALTSHTDKSAWLEAQVRQL  329

Qy  330  LQIVNQQPSRLDLRSLVDAVDSVKQRITQLEASD------QRLVLLEGETSKHDAHINI   382

Qy  340  RQ---NWE-----EADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSV 393

Qy  394  HDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKM  453
         | :| |:|:|:|:|| | | :|||| |:|| ::|:|:||  | |:|:||||| : |: |
Db  383  HKAQLNKNEERFKQLEGACYSGKLIWKVTDYRVKKREAVEGHTVSVFSQPFYTSRCGYRL  442

Qy  454  CARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKP  513
         |||:|||||| |||||||||:||: |||:|:||:|||:|:||||| || | ::|:  :|
Db  443  CARAYLNGDGSGKGTHLSLYFVVWRGEFDSLLQWPFRQRVTLMLLDQSGKKNHIVETFKA  502

Qy  514  DPNSSSFKKPTGEMNIASGCPVFVAQTVLEN---GTYIKDDTIFIKVIVDTSDLPD     566
         ||||||||:| ||||||||||:||:: :||||   :|||||||:|:||:||::|::|
Db  503  DPNSSSFKRPDGEMNIASGCPRFVSHSTLENSKNTYIKDDTLFLKVAVDLTDLED      557
```

RESULT 3
ID   O00463
AC   O00463;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF5 (TNF receptor associated factor 5).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98172745; PubMed=9511754;
RA   Mizushima S., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA   Otsuka M., Yamamoto T., Inoue J.;
RT   "Cloning and characterization of a cDNA encoding the human homolog of

RESULT 4

ID   O54896   PRELIMINARY;   PRT;   508 AA.
AC   O54896;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE   tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL   Gene 207:135-140(1998).
RN   [2]
RX   MEDLINE=97321041; PubMed=9177772;
RA   Nakano H., Shindo M., Yamada K., Yoshida M.C., Santee S.M., Ware C.F.,
RA   Jenkins N.A., Gilbert D.J., Yagita H., Copeland N.G., Okumura K.;
RT   "Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning,
RT   expression and assignment of the TRAF5 gene to chromosome 1q32.";
RL   Genomics 42:26-32(1997).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AB000509; AAC51329.1; -.
DR   EMBL; U69108; AAC51329.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE 557 AA; 64405 MW; 86EB3724CE111176 CRC64;

Query Match   39.7%; Score 1189.5; DB 4; Length 557;
Best Local Similarity   43.4%; Pred. No. 1.8e-66;
Matches 232; Conservative 112; Mismatches 170; Indels 21; Gaps 9;

```
Qy   41 KFVKTVEDRKYKCEKCRLVLCNPKQTECGHRFCESCMAALLS-SSSPPKCTACQESIIKDKV   99
Db   34 QFVERLEERYKCAFCHSVLHNPHQTGCGHRFCQHCILSLRELNTVPICPVDKVIKSQEV     93

Qy  100 FKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRK   159
Db   94 FKDNCCKREVLNLYVYCSN-APGCNAKVILGRYQDHLQ-QCLFQEVQCSNEKCREPVLRK   151

Qy  160 DLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSA   219
Db  152 DLKEHLSASCQFRKERCLYCKKDVVVINLQNHEENLCPEYPVFCPNNCA-KIILKTEVDE   210

Qy  220 HLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNE   279
Db  211 HLAVCPEAEQDCPFKHYGCAVTDKRRNLQQHEHSALREHMRLVLEKNVQLEEQISDLHKS   270

Qy  280 SVEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPF   339
Db  271 LEQKESKIQQLAETIKKLEREFKQPAQLFGKNGSFLPNIQ-VFASHIDKSAWLEAQVHQL   329

Qy  340 ------RQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSV   393
Db  330 LQMVNOQONKPDLRPLMEAVDTVKQKITLLENND------QRLAVLEEETNKHDTHINI   382

Qy  394 HDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVWGKTLSLYSQPFYTGYFGYKM   453
Db  383 HKAQLSKNEERFKLLEGTCYNGKLIWKIVIDYKMKKREAVDGHTVSIFSQSFYTSRCGYRL  442

Qy  454 CARVLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKP   513
Db  443 CARAVLNGDGSRGSHLSLYFVVMRGEFDSLLQWPFRQRVTLMLLDQ-SGKKNIMETFKP   501

Qy  514 DPNSSSFFKPTGEMNIASGCPFVVAQTVLEN--GTYIKDTIFIKVIVDTSDLPD   566
Db  502 DPNSSSFKRPDGEMNIASGCPFVAHSVLENAKNAYIKDDTLFIKVAVDLTDLED   556
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor associated factor 2A.
GN   TRAF2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=KIDNEY;
RX   MEDLINE=98129826; PubMed=9461607;
RA   Brink R., Lodish H.F.;
RT   "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2A),
RT   a TRAF2 splice variant with an extended RING finger domain that
RT   inhibits TNFR2-mediated NF-kappaB activation.";
RL   J. Biol. Chem. 273:41129-41134(1998).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF027570; AAC53545.1; -.
HSSP; P12351; 1HWT.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE 508 AA; 56757 MW; 74B8B26BFCF9B1C4 CRC64;

Query Match   27.8%; Score 832; DB 11; Length 508;
Best Local Similarity   33.6%; Pred. No. 3.3e-44;
Matches 197; Conservative 89; Mismatches 194; Indels 106; Gaps 18;

```
Qy    7 MDAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKT-VEDKYKCEKCRLVLCNPKQT    65
Db    1 MAAASVSPGSLELLQP--------GFSKTLLGTRLEAAYLCSACKNILRRPFQA        47

Qy   66 ECGHRFCESCM------AALLSSSSPK-CTAC-----QESII--KDKVFKDNCCKREI   109
Db   48 QCGHRYCSFCLTSILRCASILSSSGPQNCAACVEGLYEEGISTLLESSSAFFPDNAAREV  107

Qy  110 LALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVERAC   169
Db  108 ESLPAVCPND--GCTWKGILKEYESCHEGLCPFLLTEC--PACKGLVRLSEKEHHTEQEC  163

Qy  170 KYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS  229
Db  164 PKRSLSCQHCRAPCSHVDLEVHYEV-CPKFPLTC-DGCGKKKIPRETFODHVRACSKCRV  221

Qy  230 TCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVS------LLQNE     279
Db  222 LCRFHTVGCSEMVETENLQDHELQRLREHLALL--LSSEFLEAQASPGTLNQVGPELLQRC 279

Qy  280 SVEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPF  339
Db  280 QILEQK-IATFENIVCVLNREVER--------------VAVTAEACSRQHRLDQD----   319

Qy  340 RQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLA  399
Db  320 ----------KIEALSNKVQQLE----------------RSIGLKDLAMA          343

Qy  400 DMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVWGKTLSLYSQPFYTGYFGYKMCARVYL  459
Db  344 DLEQKVSELEVSTDGVFIWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYL   403

Qy  460 NGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSS  519
Db  404 NGDGTGRGTHLSLFFVVMKGPNDALLQWPFNQKVTLMLLDH-NNREHVIDAFRPDVTSSS  462

Qy  520 FKKPTGEMNIASGCPFVVAQTVLE-NGTYIKDDTIFIKVIVDTSDL              564
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Db   463 FQRPVSDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 508
```

RESULT 5

```
Q96NT2
ID   Q96NT2;            PRELIMINARY;      PRT;   447 AA.
AC   Q96NT2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ30124 fis, clone BRACE1000093, highly similar to TNF receptor
DE   associated factor 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RA   Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA   Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA   Kikuchi H., Kanda K., Wagatsuma M., Murakawa Y., Kanehori K.,
RA   Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA   Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AK054686; BAB70792.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 1.
DR   PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
KW   Zinc-finger.
SQ   SEQUENCE 447 AA;  49377 MW;  73E15E8346AB31D7 CRC64;

Query Match           24.3%;  Score 727.5;  DB 4;  Length 447;
Best Local Similarity 30.5%;  Pred. No. 9.4e-38;
Matches  181;  Conservative  80;  Mismatches 150;  Indels 183;  Gaps 16;

Qy    7 MDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKT-VEDKYKCEKCRLVLCNPKQT 65
          :|||  | ::::| :|   ||||  | | | : | :|  ||:||:|| || : | ||
Db    1 MAAASVTPGSLELLQP-----------GFSKTLLGTKLEAKYLCSACRNVLRRPFQA 47

Qy   66 ECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV------------FKDNCCKREILALQVYC 116
         ||||| | |: :||  ||| ::|   | :|| |            |||| |||| | |
Db   48 QCGHRYCSFCLASILSSGPQNCAACVHEGIYEBGISILESSSAFFPDNAARREVESLPAVC 107

Qy  117 RNEGRGCAEQLTLGHLLVHLKNECQFEELP--------------------------CLRAD 151
         |   ||  |                                               :
Db  108 PSD---GCTWKGTLKEYEVMPACGMVTEAPAVGSRPRSPSSYDLVLHVPLTGAEACLMSV 165

Qy  152 CKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQT 211
         ||:|    | | |     |   |: ||: :|   |
Db  166 EEFTELL--LRSCHEGRCPLMITECPACKGLVRLGEKERHLEHECPERSLSCRH-CRA-P 221

Qy  212 LLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEK 271
         ::| :|:  | |                                        || :
Db  222 CCGADVKAHEVCPKFPLTCD----GCG 247

Qy  272 KVSLLQNESVEKKKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKE 331
         |:                                                     ||
Db  248 KI------------------------------PREKFQD 256

Qy  332 LDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTL 391
         |||                                          :|:|   :
Db  257 QDK---------------------------------IEALSSKVQQLE------RSI 274
```

RESULT 6

```
Db  394 RPDVTSSSFQRPVNDMNIASGGPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 447

Q90WT6
ID   Q90WT6;            PRELIMINARY;      PRT;   501 AA.
AC   Q90WT6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Tumor necrosis factor receptor associate factor-2.
GN   TRAF2.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang T., Secombes C.J.;
RT   "Cloning and expression of crucian carp tumor necrosis factor receptor
RT   associate factor-2 (TRAF2).";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AJ297860; CAC82653.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
KW   Zinc-finger.
SQ   SEQUENCE 501 AA;  56503 MW;  DE0ED0F8D9DCC287 CRC64;

Query Match           23.6%;  Score 708;  DB 13;  Length 501;
Best Local Similarity 30.9%;  Pred. No. 1.8e-36;
Matches  160;  Conservative  86;  Mismatches 166;  Indels 106;  Gaps 14;

Qy  392 SVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGY 451
         | ||:| |||| :||| |||::| ||:|||||:| ||:|||||||| || :||:| |||
Db  275 GIKDLAMADLFQKVLEMEASTYDGVFIWKISDFAKKRQEAVAGRIPAIFSPAFYTSRYGY 334

Qy  452 KMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAF 511
         ||| |:||||| | :||||||||| | |  |||:|||:|:||||: ||: |||: :|||
Db  335 KMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQRVTLMILDQ-NNREHVIDAF 393

Qy  512 KPDPNSSSFKPTGEMNIASGCPVFVAQTVLE-NGTIYIKDTIFIKVIVDISDL 564
         :||:.||||:   :||||| | :| ::  ||    :|:||:||||:||| | |
Db  394 RPDVTSSSFQRPVNDMNIASGGPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 447

Qy   39 KEKFVKFTVEDKYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQ-ESIIKD 97
         :|: :| |  |||| | | ::| | ||: |||||| :| :||  |||| | ||  | :
Db   32 REVLSVSMEPKYCQCQQCKEILRKPFQACGHRFCVFCFKQLTSSGGPICEACRABGTFEE 91

Qy   98 KV------FKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLR 149
         |       |||| ||| | |   ||| | ||   |   |:|                 :
Db   92 AMSMLNITVAFPDNAARREIDSLPAKCPND--GCSWSGTLKDYEGQHEGRCDFERVKC-- 147

Qy  150 ADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSV 209
         | ||:|    | | |     |   |: ||: :|   |
Db  148 EACQOAVILLSEKDRHNERECEARTLNCKYCKVTFNFRKEIKAHDEI-CQKFPMQC-KDCGK 205

Qy  210 QTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLL----- 262
          ::| :|:  | |                                        || :
Db  206 KKIPREKFQEHTKSCAKKSKSACQFSEIGCRAVVDNGKQQEHQTSVMEHLRLMLSVLSSV 265

Qy  263 ------KEWNSLEKKVSLLQ-----------NKSIQSLHNQICS 296
               ||||:|||||:||||           |||:|||||:|||
Db  266 RLRAEGAGEWQE--DSGLGLYRGPEDAPPAGPNAAAHNAGRGGGPGVQOKYTALENIVCV 323

Qy  297 FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESL 356
         ::|:|| |:| |:|                                        :|
Db  324 LNREVERSALTL--------------------------------EALSRQHRLDQE 352
```

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Qy    357  QNRVTELESVSDKSAGQAARNTGLLESQLSRHHDQTLSVHDIRLADMDLRFQVLEFASYNGV  416
                |:|| : ||
Db    353  SNKVRQLE----------------------------------------------------
Qy    417  LIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVI  476
           ||||| |  |||||||||| |||||   :|||||||| | ||||||||| | ||||||:|
Db    389  FIWKIADFSRRRQDAVGGRAPAMFSPAFYSSKYGYKMCLRLYLNGDGTGRGTHLSLFFVV  448
Qy    477  MRGEYDALLPWPFFKQKVTLMLMDQGSSRRHLGDAFKPD  514
           |||:||||| ||| |||||||| ||   |||| ||| ||
Db    449  MRGKYDALLKWPFSQKVTLMLLDQ-NNREHIIDAFRPD  485
```

```
RESULT 7
ID    Q9BU24
AC    Q9BU24;
DT    01-JUN-2001 (TrEMBLrel. 17, Created)
DT    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    TNF receptor-associated factor 4.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Strausberg R.;
RL    Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC    -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR    EMBL; BC001769; AAH01769.1; -.
DR    InterPro; IPR002083; MATH.
DR    InterPro; IPR003007; TRAF.
DR    InterPro; IPR001841; Znf_ring.
DR    InterPro; IPR001293; Znf_TRAF.
DR    Pfam; PF00917; MATH; 1.
DR    Pfam; PF00097; zf-C3HC4; 1.
DR    Pfam; PF02176; zf-TRAF; 3.
DR    SMART; SM00061; MATH; 1.
DR    SMART; SM00184; RING; 1.
DR    PROSITE; PS00518; ZF_RING_1; 1.
KW    Receptor; Zinc-finger.
SQ    SEQUENCE   470 AA;  53542 MW;  A3F57E0E1081AB88 CRC64;

Query Match             18.7%;     Score 560.5; DB 4; Length 470;
Best Local Similarity   24.1%;     Pred. No. 2.6e-27;
Matches  142;  Conservative  81;  Mismatches 173;  Indels 193;  Gaps 12;
```

```
Qy   37  GYKEKFVKTVEDKYKCEKCRLVLCNPKQ-TECGHRFCESCMAALLSSSSPKCTAQESII  95
         |:||||:|  |::||:|  :||||  ||||||||:| ||| ::||  :||:|
Db    3  GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTGCGHRFCDTCLQEFLSEGVFKCPEDQLPLD  62
Qy   96  KDKVFKDNCCKREILALQVYCRNEGRCCAEQLTLGHLLIVHLKNECQFEELPC-------  147
Db   63  YAKIYPDPELEVQLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPCPNRCPMKL  121
Qy  148  ------LRADCKE----------------------------KVLRKDLR  162
Db  122  SRRDLPAHLQHDCPKRRLKCEECGCDFSGEAYESHEGMCPQESVYCENKCGARMMRLLA  181
Qy  163  DHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS  222
Db  182  QHATSECPKRTQPCTYCTKEFVPDTIQSHQ-YQCPRLPVACPNQCGVGTVAREDLPGHLK  240
Qy  223  E-CVNAPSTCSPKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWNSLEKKVSLLQNESV  281
Db  241  DSCNTALVLCPFKDSGCKHRCPKLANARHVEESVKFHLAMM------------------  281
Qy  282  EKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ  341
Db  282  -------------------CA----------------------------------  299
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Qy  342  NWEEADSMKSSVESLQNRVTELESVSDKSAGQAARNTGLLESQLSRHHDQTLSVHDIRLADM  401
Db  300  -------------------------------------------------EELSV--------  304
Qy  402  DLRFQVLEFASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNG  461
Db  305  ------GSDGVLIWKIGSVGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLNG  354
Qy  462  DGMGKGTHLSLFFVIMRGEYDALLPWPFFKQKVTLMLMDQG-----SSRRHLGDAFKPDNS  517
Db  355  NGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPNW  414
```

```
RESULT 8
ID    Q14848
AC    Q14848;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    Cystein rich domain associated to RING and TRAF protein.
GN    MLN 62, CART1.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;
RX    MEDLINE=96039245; PubMed=7490069;
RA    Tomasetto C., Regnier C.H., Moog-Lutz C., Mattei M.G., Chenard M.P.,
RA    Lidereau R., Basset P., Rio M.C.;
RT    "Identification of four novel human genes amplified and overexpressed
RT    in breast carcinoma and located to the q11-q21.3 region of chromosome
RT    17.";
RL    Genomics 28:367-376(1995).
RN    [2]
RP    SEQUENCE FROM N.A.
RC    TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;
RX    MEDLINE=96029665; PubMed=7592751;
RA    Regnier C.H., Tomasetto C., Moog-Lutz C., Chenard M.P., Wendling C.,
RA    Basset P., Rio M.C.;
RT    "Presence of a new conserved domain in CART1, a novel member of the
RT    tumor necrosis factor receptor associated protein family, which is
RT    expressed in breast carcinoma.";
RL    J. Biol. Chem. 270:25715-25721(1995).
RN    [3]
RP    SEQUENCE FROM N.A.
RC    TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;
RX    MEDLINE=98175888; PubMed=9507120;
RA    Masson R., Regnier C.H., Chenard M.P., Wendling C., Mattei M.G.,
RA    Tomasetto C., Rio M.C.;
RT    "Tumor necrosis factor receptor associated factor4 (TRAF4) expression
RT    pattern during mouse development.";
RL    Mech. Dev. 71:187-191(1998).
CC    -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR    EMBL; X80200; CAA56491.1; -.
DR    InterPro; IPR002083; MATH.
DR    InterPro; IPR003007; TRAF.
DR    InterPro; IPR001841; Znf_ring.
DR    InterPro; IPR001293; Znf_TRAF.
DR    Pfam; PF00917; MATH; 1.
DR    Pfam; PF00097; zf-C3HC4; 1.
DR    Pfam; PF02176; zf-TRAF; 3.
DR    SMART; SM00061; MATH; 1.
DR    SMART; SM00184; RING; 1.
DR    PROSITE; PS00518; ZF_RING_1; 1.
KW    Zinc-finger.
```

```
Qy  518  SSFKKP------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD  560
Db  415  KNFQKPGTWRGSLLDESSLGFGYPKFISHQDIRKRNIVRDDAVFIRAAVE  463
```

SQ SEQUENCE 470 AA; 53443 MW; 5D457E05A78770E2 CRC64;
Query Match   18.6%; Score 556.5; DB 4; Length 470;
Best Local Similarity 24.1%; Pred. No. 4.6e-27; Indels 193; Gaps 12;
Matches 142; Conservative 80; Mismatches 174;

```
Qy   37 GYKEKFVKTVEDKYKCEKCRLVLCNPKQ-TECGHRFCESCMAALLSSSSPKCTACQESII   95
Db    3 GPDYEKFLEKPKRLLCPLCGKPMREPVQVSTGGHRFCDTICLQEFLSEGVFRKCPEDQLPLD  62

Qy   96 KDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPC------    147
Db   63 YAKIYPDELEVQVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPCPNRCPMKL   121

Qy  148 -------LRADCKE------                                  KVLRKDLR 162
Db  122 SRRDLPAHLQHDCPKRLKCEPCGCGCDFSGEAVSHEGMCPQESVYCENKCGARMMRGLLA  181

Qy  163 DHVEKACKYREATCSHCKSQVPMIKLQKHEHDTDCPCVVVSCPHKCSVQTLLRSELSAHLS 222
Db  182 QHATSECPKRTQPCTYCKFEFVEDTIQSHQ-YCPRLPVACNQCGVGTVAREDLPGHLK    240

Qy  223 E-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESV  281
Db  241 DSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM                     281

Qy  282 EKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQOAEKLKELDKEIRPPRQ 341
Db  282 LVSRQROELQELRREL                                              299

Qy  300                                                     -EELSV-   304

Qy  305 -GSDGVLIWKIGSYGRRLQEEAKAKPNLECFSPAFYTHKGYKLQVSAFLNG           354

Qy  342 NWEEADSMKSSVESLQNRVTELESVDKSAGQOAARNTGLLESQLSRHDQTLSVHDIRLADM 401
Db  342 NVGSGEGTHLSLY...                                              

Qy  402 DLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPPYTGYFGYKMCARVING   461

Qy  462 DGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPNS 517
Db  355 NGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPNW  414

Qy  518 SSFKKP---------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD          560
Db  415 KNFQKPGTWRGSLDESSLGFGYPKFISHODIRKNYVRDDAVFIRAAVE              463
```

RESULT 9
ID   Q9Y4K3   PRELIMINARY;   PRT;   522 AA.
AC   Q9Y4K3;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative interleukin 1 signal transducer.
GN   TRAF6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96634892; PubMed=8837778;
RA   Cao Z., Xiong J., Takeuchi M., Kurama T., Goeddel D.V.;
RT   "TRAF6 is a signal transducer for interleukin-1.";
RL   Nature 383:443-446(1996).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; U78798; AAB38751.1; -.
HSSP; P15919; 1RMD.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.

DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ SEQUENCE 522 AA; 59573 MW; 5AB9C255CCFEE749 CRC64;
Query Match   18.3%; Score 548; DB 4; Length 522;
Best Local Similarity 26.6%; Pred. No. 1.8e-26; Indels 201; Gaps 96;
Matches 144; Conservative 101; Mismatches 201;

```
Qy   29 SVLVPEQGGYKEKFVKTVEDKYKYKCEKCGRLVLCNPKQTECGHRFCESCMAALLSSSSPKCT 88
Db   47 SSFMEEIQGYDVEFDPPLESKYECPICLMALREAVQTPCGHRFCKACIIKSIRDAGHKCP   106

Qy   89 ACQESIIKDKVFKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCL  148
Db  107 VDNEILLENQLFPDNFAKREILSLMVKCPNE--GCLHKMELRHLEDH-QAHCEFALMDC-  162

Qy  149 RADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEHDTDCPCVVVSCPHKCS 208
Db  163 -PQCQRPFQKFHINIHILKDCPRRQVSCDNCAASMAFEDKEIH-DQNCPLANVICEY-CN  219

Qy  209 VQTLLRSELSAHLS-ECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSN  267
Db  220 T-ILIREQMPNHVDLCQPTAPIPCTFSTFGCHEKMQRNHLARHLQENTQSHMRMLAQAVH  278

Qy  268 SLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQOAE 327
Db  279 SL----SVIPDSGYIS--EVNFQETHIHQLEGRLVRQDHQIRELTAKMETQSM         325

Qy  328 KLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQOAARNTGLLESQLSRH 387
Db  326 YVSELKRTR----------TLEDKVAEIEA-                               346

Qy  388 DQTLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDY----KRRKQEAVMGKTLSLYSQP  443
Db  347 ----------QQCNGIYIWKIGNEGMHLKCQEEE---KPVVIHSPG               379

Qy  444 FYTGYFGYKMCARVLN-GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG    502
Db  380 FYTGKPGYKLCMRILHLQLPTAQRCANYISLFVHTMQGEYDSHLPWPFQGTIRLTILDQSE 439

Qy  503 S--RRHLGDAFKPDPNSSSFKKPTGEMNIAS-GCPVFVAQTVLENGTYIKDDTIFIKVIV  559
Db  440 APVRQNHEEIMDAKPELLAFQRPFIPRNPKGFGYVTFMHLEALRQRIFIKDDTLLVRCEV  499
```

RESULT 10
ID   P70196   PRELIMINARY;   PRT;   530 AA.
AC   P70196;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF6.
GN   TRAF6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Inoue J.;
RT   "TRAF6, a novel CD40 associated factor.";

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Qy  560 DT 561
Db  500 ST 501
```

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RL   J. Biol. Chem. 0:0-0(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97067112; PubMed=8910514;
RA   Ishida T., Mizushima S., Azuma S., Kobayashi N., Tojo T., Suzuki K.,
RA   Aizawa S., Watanabe T., Mosialos G., Kieff E., Yamamoto T., Inoue J.;
RT   "Identification of TRAF6, a novel tumor necrosis factor receptor
RT   associated factor protein that mediates signaling from an amino
RT   terminal domain of the CD40 cytoplasmic region.";
RL   J. Biol. Chem. 271:28745-28748(1996).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; D84655; BAA12705.1; -.
DR   HSSP; P15919; 1RMD.
DR   MGD; MGI:108072; Traf6.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   530 AA;  60082 MW;  092B20B4CEDB85B CRC64;

Query Match            17.9%;  Score 535;  DB 11;  Length 530;
Best Local Similarity  25.2%;  Pred. No. 1.2e-25;
Matches 144;  Conservative 104;  Mismatches 236;  Indels 88;  Gaps 17;

Qy    3 SSKKMDAAGTLQPNPPLKLQPDRGAGSV------LVPEQGGYKEKFVKTVEDKYKCEK 54
Db   13 SQSSSDCCAAMASCSAAVKDDSVSGSASTGNLSSSFMEEIQGYDVEFDPPLESKYECPI 72

Qy   55 CRLVLCNPKQTECGHRFCESCMAALLSSSSPRCTACQESIIKDKVFKDNCCKREILALQV 114
Db   73 CLMALREAVQTPCGHRFCKACIIKSIRDAGHKCPVDNEILLENQLFPDNFAKREILSLTV 132

Qy  115 YCRNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREA 174
Db  133 KCPN--KGCLOKMELRHLEDH-QVHCEFALVNC--PQCQRPFQKCQVNTHIIEDCPRRQV 187

Qy  175 TCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS-ECVNAPSTCSF 233
Db  188 SCVNCAVSMAYEEKEIH-DQSCPLANICEY-CGT-ILIREQMPNHYDLDCPTAPIPCTF 244

Qy  234 KRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQ 293
Db  245 SVFGCHQKMQRNHLARHLQENTQLHMRLL---------------AQAVHNV 280

Qy  294 ICSFEIEIEROKEMLRNNESKILHLQRVIDSQOAEKLKELDKEIRPFRQNWEEADSMKSSV 353
Db  281 NLAL----------------RPCDAASP----SRGCRPEDPNYEE-------TI 307

Qy  354 ESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASY 413
Db  308 KOLESRLVRQDHQIRELTARMETQSMYVGELKRIIRTL----EDKVAEM-------EAQQC 357

Qy  414 NGVLIWKIRDYKRRKQEAVMGKTLSLSIYSQPFYTGYFGYKMCARVYLN-GDGMGKGTHLSL 472
Db  358 NGIYIWKIGKFGMHLKSQEERPVVIHSPGFYTGRPGYKLCMRLHLQLFPTAQRCANYISL 417

Qy  473 FFVIMRGEYDALLPWPFKQKVTLMLMDQGSS--RRHLGDAFKPDPNSSSFKKPTGEMNIA 530
Db  418 FVHTMQGEYDSHLPWPFQGTIRLTILDQSEALIRQNHEEVMDAKPELLAFQRPIPRNPK 477

Qy  531 S-GCPVFVAQTVLENGTYIKDDTIFIKVIVDT 561
Db  478 GFGYTFMHLEALRQGTFIKDDTLLVRCEVST 509
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RESULT 11
ID   Q9BIW7      PRELIMINARY;      PRT;     462 AA.
AC   Q9BIW7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   TRF-1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21407711; PubMed=11516642;
RA   Pujol N., Link E.M., Liu L.X., Kurz C.L., Alloing G., Tan M.,
RA   Ray K.P., Solari R., Johnson C.D., Ewbank J.J.;
RT   "A reverse genetic analysis of components of the Toll signaling
RT   pathway in Caenorhabditis elegans.";
RL   Curr. Biol. 11:809-821(2001).
EMBL; AF348168; AAK37546.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF01176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
SQ   SEQUENCE   462 AA;  52354 MW;  E07F04BF1756B343 CRC64;

Query Match            17.5%;  Score 523.5;  DB 5;  Length 462;
Best Local Similarity  26.2%;  Pred. No. 5.2e-25;
Matches 137;  Conservative 68;  Mismatches 188;  Indels 129;  Gaps 12;

Qy   52 CEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPRKCTACQESIIKDKVFKDNCCKREILA 111
Db   18 CPICEQALRDPIKLNCDHHYCROQCFEN--ENRTPGCAACQTIIQPELCQOHDRAKQKILA 75

Qy  112 LQVYCRNEGRGCAEQLTLGHLLVHLKNECQFE-ELPCLRADCKEKVLRKDLRDHVEKACK 170
Db   76 LPVVCTPESSGCPWDGQLGTLHDHL-SECTFKSSLKCEK--CGRQFAKNDLEKHIRAK-CE 131

Qy  171 YREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST 230
Db  132 LNRAVCSFCNKTIRDSDRERHPKT-CPQVIISCPQCGLTDRPRLEIEAHCPSCPNVDNV 190

Qy  231 CSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL 290
Db  191 CPFVPYGCTPAGGKESIOQHLSDEPVRHLMYLCDEITTDLKGTYELM--------- 236

Qy  291 HNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQOAEKLKELDKEIRPFRQNWEEADSMK 350
Db  237 -------ERDMGSFNDRQTRIL-----SAAETCTEM-- 260

Qy  351 SSVESLQNRVTELESVDKSAGQAARNTGLLESOLSRHDQTLSVHDIRLADMDLRFQVLET 410
Db  261 --------------------------------- 260

Qy  411 ASYNGVLIWKIRDYKRRKQEAVMGKTLSLSIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHL 470
Db  261 --FGPQLIWKIDIKLQQRTNEAKSGADTTIPFSVPMSHRFGYKMMACACLFGDGSSAGKSI 318

Qy  471 SLFFVIMRGEYDALLPWPFKQKVTLMLMDQGS-----SRRHLGDAFKPDPNSSSFKKPT 524
Db  319 SLYVLLKGEFDPLEWPFHRAIKISLLDQNPREDRVNITYVIDPRKLKANEKFLARPR 378

Qy  525 GEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSD-LP 565
Db  379 GERNAAFGSQSFCSLAILQN--YVKDDKIYVQIDVDRCETLP 418
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RESULT 12

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ID   062248           PRELIMINARY;    PRT;   509 AA.
AC   062248;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   F4SG2.6 protein.
GN   F4SG2.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditina;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lindsay S.J.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z93382; CAB07615.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; Znf_ring.
DR   SMART; SM00184; RING; 1.
DR   SMART; ; MATH; 1.
SQ   SEQUENCE 509 AA; 57514 MW; CFA0E068F5AD00C8 CRC64;
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Query Match   17.58;
Best Local Similarity   26.2%;
Matches 137;   Conservative 68;   Mismatches 188;   Indels 129;   Gaps 12;

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Qy    52 CEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILA 111
Db    65 CPICEQALRDPIKLNCDHHYCRQCFEN--ENRTPGCAACQTIIQPELCQHDRAKQKOILA 122

Qy   112 LQYVCRNEGRGCAEQLIGHLLVHLKNECQFE-ELPCLRADCKEKVLRKDLRDHVEKACK 170
Db   123 LPVVCTFESSGCPWDQGLGTLHDHL-SECTFKSSLKCEK--CGRQFAKNDLEKHRAK-CE 178

Qy   171 YREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST 230
Db   179 LNRAVCSPCNKITRDSDRERHKT-CPQVIISCPFQCGLTDRPRLEIEAHCPSCPNVDNV 237

Qy   231 CSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL 290
Db   238 CPFVPVYGCTFAGGKESIQOHLSDEPVRHLMYLCDEITDLKGTYELM----------- 283

Qy   291 HNQICSFEIEIEROKEMLRNNESKILHQRVIDSQAEKLKELDKEIRPFRQNWEEADSMK 350
Db   284 ----------ERDMGSPNDRQTRIL-----SAAETCTEM---------- 307

Qy   351 SSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLET 410
Db   308 ----------------- 307

Qy   411 ASYNGVLIWKIRDYKRRQEAVNGKTLSLSIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHL 470
Db   308 --FGPQLIWKIDKLQQRFNEAKSGADTIFSVPFMSHRFGYKMMACALFGDGSSAGKSI 365

Qy   471 SLFFVIMRGEYDALLPWPFKQKVTLMLMDQGS------SRRHLGDAFKPDPNSSSFKKPT 524
Db   366 SLYVLLLKGEFDPTLEWPFHRAIKISLLDQNPREDRVNITVYIDPRKLKANEKFLARPR 425

Qy   525 GERMIASGCPVFVAQTVLENGTIYIKDDTFIFIKVIVDISD-LP 565
Db   426 GERNAAFGSQSFCSLAILQN--YVRDDKIYVQIDVDRCETLP 465
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RESULT 13

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ID   Q61382           PRELIMINARY;    PRT;   470 AA.
AC   Q61382;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine rich motif associated to Ring and Traf domains protein
DE   (MCART1).
GN   TRAF4 OR CART1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98175888; PubMed=9507120;
RA   Masson R., Regnier C.H., Chenard M.P., Wendling C., Mattei M.G.,
RA   Tomasetto C., Rio M.C.;
RT   "Tumor necrosis factor receptor associated factor4 (TRAF4) expression
RT   pattern during mouse development.";
RL   Mech. Dev. 71:187-191(1998).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; X92346; CAA63103.1; -.
DR   MGD; MGI:1202880; Traf4.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE 470 AA; 53418 MW; 842F2168A926BAFB CRC64;
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Query Match   17.4%;
Best Local Similarity   23.18;
Matches 136;   Conservative 83;   Mismatches 177;   Indels 193;   Gaps 12;

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Qy    37 GYKEKFVKIVEDKYKCEKC-RLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESII 95
Db     3 GLDYKFPEKPKRRLLCPLCGKPMRDSVEVSTCGHRFCDNCLQEFLSEGVFKCPEDQLPLD 62

Qy    96 KDKVFKDNCCKREILALQVYCRNEGRGCAEQLIGHLLVHLKNECQFEELPC------ 147
Db    63 YAKIYPDPELEVVLGIAIRCIHSEEGCRWGSPLRIHLQGHL-NTCSFNVVPCPNRCPAKL 121

Qy   148 ------LRADCKE--------- 162
Db   122 SRRDLPAHLQHDCPKRLKCEFCGCDFSGEAYESHEGVCPQESVFCENKCGGARMMRRLLA 181

Qy   163 DHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS 222
Db   182 QHATSECPKRTQPCAYCTKEFVYDTIQSHQ-YQCPRLPVPCPNQCCGVGTVAREDLPTHLK 240

Qy   223 E-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESV 281
Db   241 DSCRTAFVLCPFKESGGCKHRCPKLAMGRHVEESVKPHLAMM------------ 281

Qy   282 EKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHQRVIDSQAEKLKELDKEIRPFRQ 341
Db   282 ------------------------------LVSRQRQELQELRREL------ 299

Qy   342 NWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADM 401
Db   300 --------------------------------------------EELSI------ 304
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Qy  402  DLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNG 461
         :||||| ||   ||   |||  ||| |||
Db  305  ------------GSDGVLIWIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSASLING 354

Qy  462  DGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPNS 517
         :|||  |::    |   |  ||| |     | || |||    ||:||| |:  ||
Db  355  NGSGEGTHLSIYIRVLPGAFDNLLEWPLARRVTFESLLDQSDPGLAKPQHVTETFHPDPNW 414

Qy  518  SSFKKP-------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 560
         :|:|           |||:| :|||| |||  ::|: |||:||||||:|
Db  415  KNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRASVE 463
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RESULT 14
Q9UAC5
ID   Q9UAC5;   PRELIMINARY;   PRT;   412 AA.
AC   Q9UAC5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   TRAF1.
GN   TRAF1 OR CG3048.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Richter B.W.M., Duckett C.S.;
RT   "Identification of a Drosophila TRAF homolog.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Medzhitov R., Janeway C.;
RT   "Drosophila TRAF proteins are components of innate host defense
RT   pathways.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF079837; AAD47894.1; -.
DR   EMBL; AF111422; AAG21891.1; -.
DR   FlyBase; FBgn0026319; Traf1.
DR   InterPro; IPR000083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001293; znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
SQ   SEQUENCE   412 AA; 46159 MW; 81A05147AA7D64CE CRC64;

Query Match   16.8%;   Score 500; DB 5; Length 412;
Best Local Similarity   24.9%;   Pred. No. 1.3e-23;
Matches 130; Conservative 73; Mismatches 158; Indels 162; Gaps 11;

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Qy   48  DKYKCEKCRLVLCNPKQTEGCHRFCESCMAALSSSSSPPKCTACQESIIKDKVFKDNCCKR 107
         |:|:    | ||       ::   || |  ::
Db   43  DELRLKGHLNACKHDATQCPN--------------------KCGAQIPRIMMTDHLQYCTMR 86

Qy  108  EILALQVYCRNE--GRGCAEQLTLGHLLVIHLKNECQFEELPCLRADCKEKVLRKDLRDHV 165
         ::||:     |    ||:    |::      ::   | :   |  |:| |  :|   | |  :
Db   87  RTRC--EFCQSEFSGAGLEEH------------NGSCGQEPVYC-EAKCGQRILRGRMTLHK 133

Qy  166  EKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHL-SEC 224
         |||||||||:||   |   |   |:|     |    | :|| || |    || | ::|
Db  134  SKDCAXRLRCQAHCQREFSADTLPLHA-AQCPRAPLACPQRCDAGPIPRGELEAHLRDEC 192

Qy  225  VNAPSTCSFKRYGCVPEQGTNQQIKAHEASAVQHVNLLKEWSNSLEKKVSLLQNESVEKN 284
         |  :|:   |:| || :       |  ||:|      ::    ::       |:  :| :|
Db  193  QSLAVSCSFKEAGCRFKGPRQMLEAHLESNAAHLSLMVALSSRGQQIOML------- 244

Qy  285  KSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPRQNWE 344
                                                                 -----------
Db  245  ------                                                  244
```

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Qy  345  EADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLR 404
         :|:|
Db  245  -----KSAVSKL---------------------------------------------- 251

Qy  405  FQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGM 464
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  252  -----SINYTGTLIWKIRDWSAKMAEARGKDGLELVSPPFYTSQYGYKLQASMFLNGNGP 306

Qy  465  GKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG--SSRRHLGDAFKPDPNSSSFKK 522
         |||||||||||||||||||||||||||||||||||    ||||||||||:||||| ::||
Db  307  GENTHVSYIKVLPGEYDALLKWPFSHSITFTLFEQGAQSGGGGVAESFVPDPTWENFQR 366

Qy  523  PTGEMN-IASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSDL 564
         | ::|   |||||||||||||||||||||||||||||||||||
Db  367  PSNEPDQLGFGPRFISHELLHSRPFIKGDTVFLRVKVDPSKI 409
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RESULT 15
Q9XYR0
ID   Q9XYR0;   PRELIMINARY;   PRT;   486 AA.
AC   Q9XYR0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF1 protein (LD20987p).
GN   TRAF1 OR CG3048.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).

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RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99147085; PubMed=10021364;
RA   Liu H., Su Y.C., Becker E., Treisman J., Skolnik E.Y.;
RT   "A Drosophila TNF-receptor-associated factor (TRAF) binds the ste20
RT   kinase Misshapen and activates Jun kinase.";
RL   Curr. Biol. 9:101-104(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003576; AAF51024.1; -.
DR   EMBL; AF119794; AAD34346.1; -.
DR   EMBL; AY094792; AAM11145.1; -.
DR   FlyBase; FBgn0026319; Traf1.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001293; znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
KW   Receptor.
SQ   SEQUENCE   486 AA;   53665 MW;  41474B5E014A99D5 CRC64;

Query Match             16.7%;  Score 500;  DB 5;  Length 486;
Best Local Similarity   24.9%;  Pred. No. 1.6e-23;
Matches  130;  Conservative  73;  Mismatches 158;  Indels 162;  Gaps 11;

Qy       48  DKYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQQESIIKDKVFKDNCCKR  107
             ::: ::      :                                           :   :
Db      117  DELRLKGHLNACKHDATQCPN---------------------KCGAQIPRIMMTDHLQYTCMR  160

Qy      108  EILALQYVCRNE--GRGCAEQLTLGHLLVHLKNECQFFEELPCLRADCKEKVLRKDLRDHV  165
             : ::: :             : : :            ::                ::: ::
Db      161  RTRC---EFCQSEFSGAGLEEH----------NGSCGQEPVYC-EAKCGQRILRGRMTLHK  207

Qy      166  EKACKYRFATCSHCKSQVPMIKLQKHEDTDCPCVVVSGCPHKCSVQTLLRSELSAHL-SEC  224
             : ::::       ::                 :   :: :: : :: :: :::: :  :::
Db      208  SKDCAKRLRRCAHQQREFSADTLPHA-AQCPRAPLACPQRCDAGPIPRGELEAHLRDEC   266

Qy      225  VNAPSTCSFKRYGCVFQGTNNQQIKAHERASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKN  284
             : ::    : :              :        :      ::       :: ::: :
Db      267  QSLAVSCSFKEAGCRFKGPRQMLEAHLESNAAAHLSLMVALSSRQGQQIQML-------   318

Qy      285  KSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWE  344
             : :                                         ::  ::  ::
Db      319  -----KSAVSKL-------------------------------------------------   325

Qy      345  EADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESOLSRHDQTLSVHDIRLADMDLR  404
             :    :      :::                :   :      :::  ::    :    :
Db      319  -----KSAVSKL-------------------------------------------------   325

Qy      405  FQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGM  464
             : :: :::  ::: :::  :  :::   : ::::  :::: : :::  ::: : :: ::
Db      326  -------SINYTGTLLWKITDWSAKMAEARGKDGLELVSPPFYTSQYGYKLQASMFLNGNGP  380

Qy      465  GKGTHLSLFFVIMRGEYDALLPWPFKQKVTMLMDQG--SSRRHLGDAFKPDPNSSSFKK  522
             : : :: :::  :  ::: :: :::  ::   :::    : :  : ::   ::: ::::
Db      381  GENTHVSVYIKVLPGEYDALLKWPFSHSITFTLFEQGAQSGQGGVAESFVPDTWENFQR  440

Qy      523  PTGEMN-IASGCPVFVAQQVVLENGTYIKDDTIFIKVIVDTSDL  564
             : :     :::  :: : : : : ::  :: :::: ::   ::
Db      441  PSNEPDQLGFGFPPRISHELLHSRPFIKGDTVFLRVKVDPSKI  483
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Search completed: December 19, 2002, 15:01:31
Job time : 41 secs